

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:19:59 ; search time 5588.75 Seconds
(without alignments)
11622.905 Million cell updates/sec

Title: US-09-625-573-1
Perfect score: 2232
Sequence: 1 GGATTGAAAGGAGCATT.....TATAACTATGTTGATAAAAG 2232

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:

4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_yi:*

15: em_ba:*

16: em_tun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_v1:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pai:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htg_hum:*

40: em_htg_mus:*

41: em_htg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID | Description | |
|------------|--------|-------|--------|--------|----------|---------------------|-----------------------|
| 1 | 2232 | 100.0 | 2232 | 6 | AB116074 | AR116074 Sequence 1 | |
| 2 | 2232 | 100.0 | 2232 | 6 | I79542 | I79542 Sequence 1 | |
| 3 | 2232 | 100.0 | 2232 | 9 | U03882 | U03882 Human monoc | |
| 4 | 1254 | 56.2 | 5471 | 9 | HSMCPA02 | U80924 Human monoc | |
| 5 | 1250.8 | 56.0 | 143068 | 6 | AX335952 | AX335952 Sequence | |
| 6 | 1250.8 | 56.0 | 143068 | 9 | HSU95626 | U95626 Homo sapi | |
| 7 | 1249.2 | 56.0 | 185437 | 9 | AC098613 | AC098613 Homo sapi | |
| 8 | 1068 | 47.8 | 1068 | 11 | G07339 | G07339 human SRS W | |
| 9 | 980 | 43.9 | 1979 | 6 | AR116075 | AR116075 Sequence 3 | |
| 10 | 980 | 43.9 | 1979 | 6 | I79543 | I79543 Sequence 3 | |
| 11 | 980 | 43.9 | 1979 | 9 | U03905 | U03905 Human monoc | |
| 12 | 941 | 42.2 | 1083 | 6 | AX232508 | AX232508 Sequence | |
| 13 | 939.4 | 42.1 | 1083 | 6 | AX232506 | AX232506 Sequence | |
| 14 | 939.4 | 42.1 | 1083 | 9 | D29944 | D29944 Human mRNA | |
| 15 | 937.8 | 42.0 | 1083 | 6 | AX280849 | AX280849 Sequence | |
| 16 | 937.8 | 42.0 | 1083 | 6 | E13909 | E13909 cDNA encode | |
| 17 | 889.8 | 39.9 | 1083 | 9 | AF013958 | AF013958 Macaca mu | |
| c | 18 | 816.6 | 36.6 | 2902 | AC087602 | AC087602 Pan trogl | |
| c | 19 | 672.8 | 30.1 | 1365 | 10 | RNU77349 | U77349 Rattus norv |
| c | 20 | 668.6 | 30.1 | 1364 | 10 | MMU51717 | MMU51717 Mus musculus |
| c | 21 | 668.2 | 29.9 | 10528 | 6 | AX345237 | AX345237 Sequence |
| c | 22 | 665.4 | 29.8 | 2992 | 10 | MMU56819 | U56819 Mus musculus |
| c | 23 | 663.8 | 29.7 | 1245 | 10 | MMU41035 | AF47035 Mus musculus |
| c | 24 | 643.6 | 28.8 | 1019 | 9 | AF162017 | AF162017 Cercopith |
| c | 25 | 643.6 | 28.8 | 1019 | 9 | AF162018 | AF162018 Cercopith |
| c | 26 | 643.6 | 28.8 | 1019 | 9 | AF162019 | AF162019 Cercopith |
| c | 27 | 643.6 | 28.8 | 1019 | 9 | AF162029 | AF162029 Cercopith |
| c | 28 | 643.6 | 28.8 | 1019 | 9 | AF162030 | AF162030 Cercopith |
| c | 29 | 643.6 | 28.8 | 1059 | 9 | AF035222 | AF035222 Cercopith |
| c | 30 | 643.6 | 28.8 | 1059 | 9 | AF081577 | AF081577 Cercopith |
| c | 31 | 643.6 | 28.8 | 1075 | 9 | AF019379 | AF019379 Cercopith |
| c | 32 | 642 | 28.8 | 1019 | 9 | AF162006 | AF162006 Cercopith |
| c | 33 | 642 | 28.8 | 1019 | 9 | AF162038 | AF162038 Cercopith |
| c | 34 | 642 | 28.8 | 1019 | 9 | AF162040 | AF162040 Cercopith |
| c | 35 | 642 | 28.8 | 1059 | 9 | AF075448 | AF075448 Pygathrix |
| c | 36 | 642 | 28.8 | 1059 | 9 | AF177884 | AF177884 Hylobates |
| c | 37 | 642 | 28.8 | 1086 | 9 | CAU83324 | U83324 Cercopithec |
| c | 38 | 642 | 28.8 | 1086 | 9 | CAU83325 | U83325 Cercopithec |
| c | 39 | 640.4 | 28.7 | 1019 | 9 | AF161957 | AF161957 Macaca fu |
| c | 40 | 640.4 | 28.7 | 1019 | 9 | AF162022 | AF162022 Cercopith |
| c | 41 | 640.4 | 28.7 | 1019 | 9 | AF162023 | AF162023 Cercopith |
| c | 42 | 640.4 | 28.7 | 1019 | 9 | AF162027 | AF162027 Cercopith |
| c | 43 | 640.4 | 28.7 | 1019 | 9 | AF162031 | AF162031 Cercopith |
| c | 44 | 640.4 | 28.7 | 1019 | 9 | AF162037 | AF162037 Cercopith |
| c | 45 | 640.4 | 28.7 | 1019 | 9 | AF162041 | AF162041 Cercopith |

ALIGNMENTS

| RESULT 1 | AR116074 | LOCUS | Sequence 1 | from patent | 2232 bp | DNA |
|--|----------|------------|------------|-------------|-------------|-----|
| DEFINITION | | DEFINITION | | US 6132987. | | |
| ACCESSION | AR116074 | ACCESSION | AR116074 | AR116074 | GI:14096396 | |
| VERSION | | VERSION | | | | |
| KEYWORDS | | KEYWORDS | | | | |
| SOURCE | | SOURCE | | | | |
| ORGANISM | | ORGANISM | | | | |
| REFERENCE | | REFERENCE | | | | |
| AUTHORS | | AUTHORS | | | | |
| TITLE | | TITLE | | | | |
| | | | | | | |
| 1. (bases 1 to 2232) | | | | | | |
| Recombinant mammalian monocyte chemotactic protein-1 (MCP-1) | | | | | | |
| Receptors (MCP-1R, CCR-2) | | | | | | |
| Patent: US 6132987-A 1 17-OCT-2000; | | | | | | |
| JOURNAL | | | | | | |

Pred. No. is the number of results predicted by chance to have a

| FEATURES | Location/Qualifiers |
|------------|--|
| source | 1..2232 |
| BASE COUNT | 602 a |
| ORIGIN | /organism="unknown" 0; Mismatches 2232; Conservative 464 c 508 g |
| QY | 1 GAACTGAAAGGACGCAATTCCCCAGTACAT |
| Db | 1 GGATTGAAAGACGCAATTCCCCAGTACAT |
| QY | 61 CGGTTATGAAATAACCAACAGAGGGTGG |
| Db | 61 CGGTTATGAAATAACCAACAGAGGGTGG |
| QY | 121 TAGGGTGTCCGTCAATTGTCATAAATTGACGTGA |
| Db | 121 TAGGGTGTCCGTCAATTGTCATAAATTGACGTGA |
| QY | 181 CCTACTGCTGTGTCATCTTGGTTTG |
| Db | 181 CCTACTGCTGTGTCATCTTGGTTTG |
| QY | 241 ATAAACTGCAAAAGCTGAAGTGTGACTGA |
| Db | 241 ATAAACTGCAAAAGCTGAAGTGTGACTGA |
| QY | 301 GATCTGTGTTTCTTATTACTCTCCATTGTC |
| Db | 301 GATCTGTGTTTCTTATTACTCTCCATTGTC |
| QY | 361 TTGGGAATGCAATGTCGAATTATTCACAGG |
| Db | 361 TTGGGAATGCAATGTCGAATTATTCACAGG |
| QY | 421 ATCTTCTTCATCTCCCTGACAATGCAATGATAG |
| Db | 421 ATCTTCTTCATCTCCCTGACAATGCAATGATAG |
| QY | 481 GCTTTAAAGCAGACGTCACCTTGGGT |
| Db | 481 GCTTTAAAGCAGACGTCACCTTGGGT |
| QY | 541 GCTGTGTTGCTCTGTCCTCCAGGAATCACTTC |
| Db | 541 GCTGTGTTGCTCTGTCCTCCAGGAATCACTTC |
| QY | 601 TATGTCCTGGCCCTTATTTCAAGGATGGATGCC |
| Db | 601 TATGTCCTGGCCCTTATTTCAAGGATGGATGCC |
| QY | 661 ATTTGGGTGSGTCCTGCGCTCTCATCAT |
| Db | 661 ATTTGGGTGSGTCCTGCGCTCTCATCAT |
| QY | 721 ACCCTGCTTCGGTGTGAAACGAAAGAGGG |
| Db | 721 ACCCTGCTTCGGTGTGAAACGAAAGAGGG |
| QY | 781 ATCATGATGTTACTTCTCTGGAATCTCC |
| Db | 781 ATCATGATGTTACTTCTCTGGAATCTCC |
| QY | 841 TTGGGAAATCTGGCTGTGAACTGTGA |
| Db | 841 TTGGGAAATCTGGCTGTGAACTGTGA |
| QY | 901 CAGTGACAGACGACTCTGGATGACTCACTG |
| Db | 901 CAGTGACAGACGACTCTGGATGACTCACTG |

| | | | |
|----|------|--|------|
| Qy | 961 | GTGGGGAGAGTTAGAGGCTTTTCACATAGCTCTGGCTGTAGGATTGCCCACTC | 1020 |
| Db | 961 | GTGGGGAGAGTTAGAGGCTTTTCACATAGCTCTGGCTGTAGGATTGCCCACTC | 1020 |
| Qy | 1021 | CAAAACCACTGTGGAGGTCCAGGAGTGGACCAAGAAAGTGTGAAAGTGTACCA | 1080 |
| Db | 1021 | CAAAACCACTGTGGAGGTCCAGGAGTGGACCAAGAAAGTGTGAAAGTGTACCA | 1080 |
| Qy | 1081 | CAAGGACATCTCGATGTGGTGGAAAAGTCATGGCAGAGCCCTGAGGCCAGT | 1140 |
| Db | 1081 | CAAGGACATCTCGATGTGGTGGAAAAGTCATGGCAGAGCCCTGAGGCCAGT | 1140 |
| Qy | 1141 | CTTCAGGACAAAGAGGAGCCTAGAGACAGAAATGACAATCTGTGTTGGAAATACA | 1200 |
| Db | 1141 | CTTCAGGACAAAGAGGAGCCTAGAGACAGAAATGACAATCTGTGTTGGAAATACA | 1200 |
| Qy | 1201 | CGCTGTGGCTCACATGGTGAATCACAGTGTGCAATCTGGGTCATGTTACAGGCA | 1260 |
| Db | 1201 | CGCTGTGGCTCACATGGTGAATCACAGTGTGCAATCTGGGTCATGTTACAGGCA | 1260 |
| Qy | 1261 | GGAGGGCTGAGGGAGAGACCTCCAGCTGGGTGAGAAAACAGTATTTCACACTCT | 1320 |
| Db | 1261 | GGAGGGCTGAGGGAGAGACCTCCAGCTGGGTGAGAAAACAGTATTTCACACTCT | 1320 |
| Qy | 1321 | TCCAGTTCCTCATTTGAAATACAGGCAATAGCTCACACTTTTAAATGAAAT | 1380 |
| Db | 1321 | TCCAGTTCCTCATTTGAAATACAGGCAATAGCTCACACTTTTAAATGAAAT | 1380 |
| Qy | 1381 | AAAATPAAGCTGAAACTGCAACTTAAATGGPAAAGCTTAAATGGTGTGTGTAT | 1440 |
| Db | 1381 | AAAATPAAGCTGAAACTGCAACTTAAATGGPAAAGCTTAAATGGTGTGTGTAT | 1440 |
| Qy | 1441 | CATGTCAAACCTGAAATGGTCAATTAGTCAGAGATAATTCAGCTTGGCTTAAGA | 1500 |
| Db | 1441 | CATGTCAAACCTGAAATGGTCAATTAGTCAGAGATAATTCAGCTTGGCTTAAGA | 1500 |
| Qy | 1501 | ATTTTGAAGCAGGTGGTGAATGGQAQACTGCTGAGTCACCCAAATGGTGTGATGGC | 1560 |
| Db | 1501 | ATTTTGAAGCAGGTGGTGAATGGQAQACTGCTGAGTCACCCAAATGGTGTGATGGC | 1560 |
| Qy | 1561 | AGGAGTGGAAAGTGTGATCTGGCAGCATCTAGCTGGCATCTAGTGTAGTA | 1620 |
| Db | 1561 | AGGAGTGGAAAGTGTGATCTGGCAGCATCTAGCTGGCATCTAGTGTAGTA | 1620 |
| Qy | 1621 | ATGATGTCGTTGAATCACACTATAGCTCATTCTGGCTCATTCAGTGTCTCATT | 1680 |
| Db | 1621 | ATGATGTCGTTGAATCACACTATAGCTCATTCTGGCTCATTCAGTGTCTCATT | 1680 |
| Qy | 1681 | CTCTCAGGCTTGTGTCGCAAAAGGCCCTTGTGTTTGTTGTTGATCATATGAGTCATGC | 1740 |
| Db | 1681 | CTCTCAGGCTTGTGTCGCAAAAGGCCCTTGTGTTTGTTGTTGATCATATGAGTCATGC | 1740 |
| Qy | 1741 | CTTTAATCACATTGGAGTTCACTGCTGGAAAGCTCCCTGAAAGTAAAGCTTCTCTAGT | 1800 |
| Db | 1741 | CTTTAATCACATTGGAGTTCACTGCTGGAAAGCTCCCTGAAAGTAAAGCTTCTCTAGT | 1800 |
| Qy | 1801 | CTAAATTGGCAGTGGAAACTCCCTAAATCAAATTGGCTCTTAATCAAGCTTTAAACCT | 1860 |
| Db | 1801 | CTAAATTGGCAGTGGAAACTCCCTAAATCAAATTGGCTCTTAATCAAGCTTTAAACCT | 1860 |
| Qy | 1861 | ATTGGTAAGAAATGGAAAGTGGCAACTTGGAAACTGCTCAAGCTTCTCTAGT | 1920 |
| Db | 1861 | ATTGGTAAGAAATGGAAAGTGGCAACTTGGAAACTGCTCAAGCTTCTCTAGT | 1920 |
| Qy | 1921 | CGGCCAAGTTAGAACTTGTGTCGCCAGTGTGCTGATCTGGCTGAAAGCTTCAAGCAG | 1980 |
| Db | 1921 | CGGCCAAGTTAGAACTTGTGTCGCCAGTGTGCTGATCTGGCTGAAAGCTTCAAGCAG | 1980 |
| Qy | 1981 | AAACACTGGCTCTAGAACCCAGGCAACTTGGAAACTGACTCCAAACTGGGACTATGGC | 2040 |
| Db | 1981 | AAACACTGGCTCTAGAACCCAGGCAACTTGGAAACTGACTCCAAACTGGGACTATGGC | 2040 |

| | | | |
|-----------------------|--|---|---------------|
| Qy | 2041 | TCTACTTCTCAGGCCACATGGCTAAAGAGGTTCTAGAAAGAGTGGGACAGAGAAC | 2100 |
| db | 2041 | TCTACTTCTCAGGCCACATGGCTAAAGAGGTTCTAGAAAGAGTGGGACAGAGAAC | 2100 |
| Qy | 2101 | TTCACCTCATATATTGTATGATCCTAATGAACTAAATGTAAGTGTGTTGAA | 2160 |
| Db | 2101 | TTCACCTCATATATTGTATGATCCTAATGAACTAAATGTAAGTGTGTTGAA | 2160 |
| Qy | 2161 | TGAAATGTTAAACTGTTTAACACTATGATTGGAAAATAATCAATGCTATAACTA | 2220 |
| Db | 2161 | TGAAATGTTAAACTGTTTAACACTATGATTGGAAAATAATCAATGCTATAACTA | 2220 |
| Qy | 2221 | TGTTGATAAAAG 2232 | |
| Db | 2221 | TGTTGATAAAAG 2232 | |
| RESULT 2 | | | |
| LOCUS | 179542 | 179542 2232 bp DNA | linear |
| DEFINITION | Sequence 1 from patent US 5707815. | | PAT 10-JUN-11 |
| ACCESSION | 179542 | | |
| VERSION | 179542.1 | GI:3207832 | |
| KEYWORDS | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 2232) | | |
| AUTHORS | Charo, I.F. and Coughlin, S.R. | | |
| TITLE | Mammalian monocyte chemoattractant protein receptors and assays using them | | |
| JOURNAL | Patent: US 5707815-A 1 13-JAN-1998; | | |
| FEATURES | Location/Qualifiers | | |
| SOURCE | 1. .2232 /organism="unknown" | | |
| BASE COUNT | 602 a 464 c 508 g 658 t | | |
| ORIGIN | | | |
| Query Match | 100.0% | Score 2232; | DB 6; |
| Best Local Similarity | 100.0% | Pred. No. 0; | Length 2232; |
| Matches 2232; | Conservative 0; | Mismatches 0; | Indels 0; |
| Gaps | | | |
| Qy | 1 | GGATTGAACTAGGGACATTCCCAAGTACATCCAAACATGCTTCACATCGTCTCT | 60 |
| Db | 1 | GGATTGAACTAGGGACATTCCCAAGTACATCCAAACATGCTTCACATCGTCTCT | 60 |
| Qy | 61 | CGGTTATCAGAAATACCAACGAGGGTGAAGAGTCACCCCTTTGATATTGAT | 120 |
| Db | 61 | CGGTTATCAGAAATACCAACGAGGGTGAAGAGTCACCCCTTTGATATTGAT | 120 |
| Qy | 121 | TACGGTGTCCCTGTTGAAATAATTGACCTGAAAGCAAATTGGGGCCAAACTCTGCTCCG | 180 |
| Db | 121 | TACGGTGTCCCTGTTGAAATAATTGACCTGAAAGCAAATTGGGGCCAAACTCTGCTCCG | 180 |
| Qy | 181 | CTCTACTCGCTGGTGTCACTTGGGAACTGCTGCTCTCATCTTA | 240 |
| Db | 181 | CTCTACTCGCTGGTGTCACTTGGGAACTGCTGCTCTCATCTTA | 240 |
| Qy | 241 | ATAAACTGCAAAAAGCTGAAGTCAGTCATTCACCTGCTCAACCTGCCATCTCT | 300 |
| Db | 241 | ATAAACTGCAAAAAGCTGAAGTCAGTCATTCACCTGCTCAACCTGCCATCTCT | 300 |
| Qy | 301 | GATCTCTTCTTCTTACTCTCCATTGCGGCTCACTCTGCTCAATGTTGGTC | 360 |
| Db | 301 | GATCTCTTCTTCTTACTCTCCATTGCGGCTCACTCTGCTCAATGTTGGTC | 360 |
| Qy | 361 | TTGGGATGCAATTGCAATTGCTGCTATTGCTCATCGTTATTGGGGA | 420 |
| Db | 361 | TTGGGATGCAATTGCAATTGCTGCTATTGCTCATCGTTATTGGGGA | 420 |
| Qy | 421 | ATCTCTTCATCATCTCTGCAATTGCTGCTATTGCTCATCGTTGTT | 480 |
| Db | 421 | ATCTCTTCATCATCTCTGCAATTGCTGCTATTGCTCATCGTTGTT | 480 |

| | | | |
|------------|--|---|--|
| QY | 1561 AGGAGTTGGAAGTGTGTGATCTGTGGCACATTAGCCTATGTCATGCAAGGATCTAAAGTA 1620 | JOURNAL | Submitted (01-DEC-1993) Scott J. Myers, Cardiovascular, The Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110, USA |
| Db | 1561 AGGAGTTGGAAGTGTGTGATCTGTGGCACATTAGCCTATGTCATGCAAGGATCTAAAGTA 1620 | FEATURES | Location/Qualifiers |
| QY | 1621 ATGATGTCGTTGAACTCACAGTATACGCTCCATGCTGTCATCTCAGCTTCATT 1680 | source | 1..2232 |
| Db | 1621 ATGATGTCGTTGAACTCACAGTATACGCTCCATGCTGTCATCTCAGCTTCATT 1680 | | /organism="Homo sapiens" |
| QY | 1681 CTCTCAGGGTGTGCGCCAAAGGCCCTTGTGTTGTATCATTAGTCAGTCATGC 1740 | | /db_xref="taxon: 9606" |
| Db | 1681 CTCTCAGGGTGTGCGCCAAAGGCCCTTGTGTTGTATCATTAGTCAGTCATGC 1740 | | /clone="ccr2-9a" |
| QY | 1741 GTTAAATCACATTCGAGTTCACTGTCAGTCAGTCCTGATGTCATATGTTCC 1800 | | /cell_line="Monomac 6" |
| Db | 1741 GTTAAATCACATTCGAGTTCACTGTCAGTCAGTCCTGATGTCATATGTTCC 1800 | | /clone_lib="Monomac6 #-3" |
| QY | 1801 CTAATTGGCAGTGGAAACTCCCTAAATCAAAATGGCTCTTAATCAAAGCTTTAAACCT 1860 | | 40..1164 |
| Db | 1801 CTAATTGGCAGTGGAAACTCCCTAAATCAAAATGGCTCTTAATCAAAGCTTTAAACCT 1860 | | /standard_name="monocyte chemoattractant protein 1 receptor" |
| QY | 1861 ATTTGGTAAGAAATGGAAAGCTGGAGAAGGCTCCCGAAAGTAGCAAGAACACTTCCCTCTTGTAGT 1920 | | /note="alternatively spliced; MCP-1RA" |
| Db | 1861 ATTTGGTAAGAAATGGAAAGCTGGAGAAGGCTCCCGAAAGTAGCAAGAACACTTCCCTCTTGTAGT 1920 | | /codon_start=1 |
| QY | 1921 CGAGCCAAGTTAAGAATGTTCTATGTTGCCAAGTGTTCTGATCAGTCAGCAAGCAAG 1980 | | /product="MCP-1 receptor" |
| Db | 1921 CGAGCCAAGTTAAGAATGTTCTATGTTGCCAAGTGTTCTGATCAGTCAGCAAGCAAG 1980 | | /protein_id="PAA1919_1" |
| QY | 1981 AACACTGGCCTCTAGACCGGAACACTGGAAACTAGACTCCAAAGCTGGCATATGCC 2040 | | /db_xref="GI: 472556" |
| Db | 1981 AACACACGGGCCTCTAGACCGGAACACTGGAAACTAGACTCCAAAGCTGGCATATGCC 2040 | | /translation="MLSTRSRSPRIRNTNESGEEVTFDYYDGCAPCHKEVDVKOIGAQL |
| QY | 2041 TCTACCTTCAGGCCACATGGTAAAGAAGTGGTCAAGAAAGTCACAGGAGAAC 2100 | | LPPPLSUVFIRFEGVNMNLYVILINCKKLKCTDIYLNLNAISDLEFLTLPWAHSA |
| Db | 2041 TCTACCTTCAGGCCACATGGTAAAGAAGTGGTCAAGAAAGTCACAGGAGAAC 2100 | | ANLWFGCNAACKLFLGKHFGLHIGFGVFLKRYLAVHFAKLRTVLPGVVTT |
| QY | 2101 TTTCACCTTCATATTTGTATGATCCTATGAAATGTTAATGTGATGTTGA 2160 | | SVTFLWAVFAASVPGILFPTKQCODESYVVGPFPRGRNNFHTTMRLNGLVPLLMM |
| Db | 2101 TTTCACCTTCATATTTGTATGATCCTATGAAATGTTAATGTGATGTTGA 2160 | | CESTSOLODQATQYTFETLGMTHCCINPLIYAFGKFRSLPHIALGCRTAPLQRPVCGG |
| QY | 2161 TGAATGTTAAATFACTGTTTAAACACTGATTGAAATTAAATCAATGTTAAACTA 2220 | BASE COUNT | 602 a 464 c 508 g 658 t |
| Db | 2161 TGAATGTTAAATFACTGTTTAAACACTGATTGAAATTAAATCAATGTTAAACTA 2220 | ORIGIN | |
| QY | 2221 TGTGATAAAAG 2232 | | |
| Db | 2221 TGTGATAAAAG 2232 | | |
| RESULT 3 | HSU03882 | mRNA | linear |
| LOCUS | HSU03882 | 2232 bp | PRI 22-JUN-1994 |
| DEFINITION | Human monocyte chemoattractant protein 1 receptor (MCP-1RA) | | |
| ACCESSION | U03882 | alternatively spliced mRNA, complete cds. | |
| VERSION | U03882.1 | GI:472555 | |
| SOURCE | human | | |
| ORGANISM | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| REFERENCE | 1. (bases 1 to 2232) | | |
| AUTHORS | Charo, I. F., Myers, S. J., Herman, A., Franci, C., Connolly, A. J. and Coughlin, S. R. | | |
| TITLE | Monocytic chemoattractant protein 1 receptors reveal alternative splicing of the carboxyl-terminal tails | | |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994) | | |
| MEDLINE | 9419581 | | |
| PUBMED | 8146186 | | |
| REFERENCE | 2 (bases 1 to 2232) | | |
| AUTHORS | Myers, S. J. | | |
| TITLE | Direct Submission | | |

| | | | | |
|------------|---|---|---------------|---|
| mRNA | tail" | 1555 | .3496 | /product="monocyte chemoattractant protein 1 receptor" |
| | /note="monocyte chemoattractant protein 1 receptor with B-form carboxyl tail" | | | /note="alternatively spliced form with B-form carboxyl tail" |
| CD5 | tail". 2546 .3756 .3939 | | | /note="MCP-1RA receptor; alternatively spliced form including A-form carboxyl tail" |
| | /codon_start=1 | | | /product="monocyte chemoattractant protein 1 receptor" |
| | /protein_id="AAC51637.1" | | | /db_xref="GI 1816525" |
| | /transliteration="MLSTSRSETRNTNESGEVTTFFDYDGAPEKHDVKQIGLPPILSFLVIFGEGVNMVFLVLTILNCKLKLCLDYLNLNAISDLEFLLTLPWIAANWFGNAMCKLFTGLYHIGYGGTCACTTCTTIDYLWLNVHAFATVTPG | | | |
| | SVITWLAVAFASVPG.1.IFTKQREDSVYVCGPYPFRGWNHETIMRNLTGLVLPV | | | |
| | VICYSGLKTLRCKRNEKKHRARRVVIETMIVYFLWTPYNNVIVLNLNPEQEFCS | | | |
| | CESTQSDQATOVTETLGMTKHCINPLIYKAVFERSLPHALGCRJAPLQKEPV | | | |
| | PYVRPGKAKVKTIVTQGLLDRGKESKGIAPEASQIDKEGA." | | | |
| CD5 | 1606 .2688 | | | /note="MCP-1RB receptor; alternatively spliced form including B-form carboxyl tail" |
| | /codon_start=1 | | | /product="monocyte chemoattractant protein 1 receptor" |
| | /protein_id="AAC51636.1" | | | /db_xref="GI 173034" |
| | /transliteration="MLSTSRSETRNTNESGEVTTFFDYDGAPEKHDVKQIGLPPILSFLVIFGEGVNMVFLVLTILNCKLKLCLDYLNLNAISDLEFLLTLPWIAANWFGNAMCKLFTGLYHIGYGGTCACTTCTTIDYLWLNVHAFATVTPG | | | |
| | SVITWLAVAFASVPG.1.IFTKQREDSVYVCGPYPFRGWNHETIMRNLTGLVLPV | | | |
| | VICYSGLKTLRCKRNEKKHRARRVVIETMIVYFLWTPYNNVIVLNLNPEQEFCS | | | |
| | CESTQSDQATOVTETLGMTKHCINPLIYKAVFERSLPHALGCRJAPLQKEPV | | | |
| | PYVRPGKAKVKTIVTQGLLDRGKESKGIAPEASQIDKEGA." | | | |
| CD5 | 1540 a 1127 c 1324 g 1480 t | | | |
| | | | | |
| BASE COUNT | | | | |
| ORIGIN | | | | |
| | | | | |
| Query | Match | 56.28 | Score 1254 | /db 9; Length 5471; |
| | Best Local Similarity | 100.0% | Pred. No. 0; | |
| | Matches 1254; | Conservative | Mismatches 0; | |
| | | | Indels 0; | |
| | | | Gaps 0; | |
| Qy | 979 | AGCCCTTTACATAGCTCTGGCTGTAGATTGCCCACTCCAAAACCACTGTTGCGA 1038 | | |
| Db | 3754 | AGCCCTTTACATAGCTCTGGCTGTAGATTGCCCACTCCAAAACCACTGTTGCGA 3813 | | |
| Qy | 1039 | GGTCAGAGTAGACAGAGAAAGATGTGAAGTGTACTACAAGGACTCTCGATGGT 1098 | | |
| Db | 3814 | GGTCAGAGTAGACAGAGAAAGATGTGAAGTGTACTACAAGGACTCTCGATGGT 3873 | | |
| Qy | 1099 | CCTGAAAGAAAGCAATTGCAAGGCCCTGTGAGCCAGCTTCTGGACAAGAGGA 1158 | | |
| Db | 3874 | CCTGAAAGAAAGCAATTGCAAGGCCCTGTGAGCCAGCTTCTGGACAAGAGGA 3933 | | |
| Qy | 1159 | GCCTAGACAGAAATGACAGATCTGGCTTGGAAATCACGTCTGGCTCACAGATG 1218 | | |
| Db | 3934 | GCCTAGACAGAAATGACAGATCTGGCTTGGAAATCACGTCTGGCTCACAGATG 3993 | | |
| Qy | 1219 | TGTGATTCAAGTAGCTGGTACATCTGGTCTACGGAGGAAGCTGAGAGGAG 1278 | | |
| Db | 3994 | TGTGATTCAAGTAGCTGGTACATCTGGTCTACGGAGGAAGCTGAGAGGAG 4053 | | |
| Qy | 1279 | AGACTCAGCTGGTGGTGGAAACACTATTCCAAACTTACCTTCCAGTTCTCATTTTG 1338 | | |
| Db | 4054 | AGACTCAGCTGGTGGTGGAAACACTATTCCAAACTTACCTTCCAGTTCTCATTTTG 4113 | | |
| Qy | 1339 | AATACAGGCTAGAGCTAGACTTTTAATAGTAAATAATAAAGCTGAAAC 1398 | | |
| Db | 4114 | AATACAGGCTAGAGCTAGACTTTTAATAGTAAATAATAAAGCTGAAAC 4173 | | |
| Qy | 1399 | TGCAACTGTAATGTTGAAAGAGTTAGTTGCTACATGTCAAACGTGAAAT 1458 | | |
| Db | 4174 | TGCAACTGTAATGTTGAAAGAGTTAGTTGCTACATGTCAAACGTGAAAT 4233 | | |
| Qy | 1459 | GCCTATAGTCAGAGATAATCTAGCTTGGACTAAAGTTCAGCTTGGAGCTGAAAT 1518 | | |

| BASE COUNT | 41194 | /db_xref="taxon:91606" | Db | 49213 | TTCTTATGTTGCCACTGTGTTCTGATCTGAGCAAGAACACTGGCTCTAGA 49272 | | |
|-----------------------|---|--|-----------|-----------------|--|--|--|
| ORIGIN | a 30122 c 3203 g 39349 t | | QY | 1999 | ACCGGAACCTGGAACTAGACTGACTCCAAAGCTGGACTATGGCTTACTTTCAGGCCACAT 2058 | | |
| Query Match | 56.0% | Score 1250.8; | DB | 6; | Length 143068; | | |
| Best Local Similarity | 99.8% | Pred. No. 0; | Db | 49273 | ACCGGAACCTGGAACTAGACTGACTCCAAAGCTGGACTATGGCTTACTTTCAGGCCACAT 49332 | | |
| Matches 1252; | Conservative 0; | Mismatches 2; | Indels 0; | Gaps 0; | | | |
| QY | 979 | AGCCTTTTCATAGTCCTGCTGGCTTGGATGTTGAGTGTGGA 1038 | QY | 2059 | GCCTAAAGAAGTTCTGAAAGAAGTGGAGAGAGAACTTCACTTCATATATT 2118 | | |
| Db | 48253 | AGCCTTTTCATAGTCCTGCTGGCTTGGATGTTGAGTGTGGA 48312 | Db | 49333 | GCCTAAAGAAGTTCTGAAAGAAGTGGAGAGAGAACTTCACTTCATATATT 49392 | | |
| QY | 1039 | GTTCCAGAGTGAGCCAGAACCTCCAGTGTGATGT 1098 | QY | 2119 | GTATGATCCTTAATGAACTGCTTAAATGTTAATGTGAAATGCTGT 2178 | | |
| Db | 48313 | GTCAGAGTGAGCCAGAACCTCCAGTGTGATGT 48372 | Db | 49393 | GTATGATCCTTAATGAACTGCTTAAATGTTAATGTGAAATGCTGT 49452 | | |
| QY | 1099 | CCTGGAAAAGGAAACTCAATTGGAGCCCTGTGAGCAAAAGAGGA 1158 | QY | 2179 | TTAACAACTATGTTGGAAAATAAATCAATCTTAACTGTGTTGATAAAAG 2232 | | |
| Db | 48373 | CCTGGAAAAGGAAACTCAATTGGAGCCCTGTGAGCAAAAGAGGA 48432 | Db | 49453 | TTAACAACTATGTTGGAAAATAAATCAATCTTAACTGTGTTGATAAAAG 49506 | | |
| RESULT 6 | | | | | | | |
| LOCUS | HSU95626 | 143068 bp | DNA | PRI 16-MAY-1997 | | | |
| DEFINITION | Homo sapiens ccr2b (ccr2), ccr4 (ccr2), ccr5 (ccr5) and ccr6 (ccr6) gene, complete cds, and lactotferrin (lactotferrin) gene. | | | | | | |
| ACCESSION | U95626 | | | | | | |
| VERSION | U95626.1 | | | | | | |
| SOURCE | U95626.1 (bases 1 to 143068) | | | | | | |
| ORGANISM | Homo sapiens | | | | | | |
| REFERENCE | 1 (bases 1 to 143068) | | | | | | |
| AUTHORS | McCombie, W.R., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D., Nhan, M., Parnell, L., Dehdia, N., Ansari, A., Mardis, E., Schutz, K., Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J., Muzy, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, L.E., Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D., and Sargianni, J.-L. | | | | | | |
| TITLE | Human BAC clone 110P12 | | | | | | |
| JOURNAL | Unpublished (1997) | | | | | | |
| COMMENT | 2 (bases 1 to 143068) | | | | | | |
| AUTHORS | McCombie, W.R., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D., Nhan, M., Parnell, L., Dehdia, N., Ansari, A., Mardis, E., Schutz, K., Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J., Muzy, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, L.E., Solinsky, K.A., Desilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D., and Sargianni, J.-L. | | | | | | |
| JOURNAL | Direct Submission | | | | | | |
| COMMENT | Submitted (27 MAR-1997) Advanced Genome Sequence Analysis Course, Cold Spring Harbor Laboratory, 1Bungtown Rd., Cold Spring Harbor, NY 11724, USA | | | | | | |
| FEATURES | Regions with single-strand coverage are as follows: | | | | | | |
| source | /organism="Homo sapiens" | | | | | | |
| | /db_xref="taxon:9606" | | | | | | |
| | /chromosome="3" | | | | | | |
| | /clone="BAC 110P12" | | | | | | |
| | /gene="ccr2" | | | | | | |
| | /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) mRNA (Accession Number U80934), two alternatively spliced mRNAs." | | | | | | |

| | |
|------------|---|
| gene | /evidence="not_experimental" 96642 . . 97676 |
| CDS | /gene="ccr6" 96642 . . 97676 |
| | /note="Identified as a gene by Graffl Version 1.3C. Translated sequence exhibits 42% sequence identity to CCR5 protein." |
| gene | /codon_start=1 /evidence="not_experimental" /product="ccr6" /protein_id="AAAB57794.1" /db_xref="GT:2104521" /translation="MANYLTAPEDEVDYEGELESDAEQCDKYDQAQLSAQLYPSL CSAVFVGVLNDLNLVLLVAKVKGKLRVNIYLLNLAVSNLCKFLTLTPWAHGDPM CKLIGLYGLYSETFVNCLLVEVQRYLVFLHGKNEFSARRYCGITSLVSLVANVY LATLPEVYVKEPOMEDQYKCAFSRTPPLPADETFWKFLTLKTMNISVVLPLFTE LYVOMRTELREFEQRYSLFVLYEAIMVYLLMPPAANAEFLSTFKEHSLSDCKSSY NLDSKWHITKLIAFHCCINPLLYAFLDGTFSKYLRCRCHLRSNTPLQRGQSAGTS REBPDHSVE" |
| gene | complement(124605 . .>139255) /note="lactoferrin" complement(join(124605 . .124816 . .126528 . .126717, 127884 . .128068 . .130006 . .130073 . .132023 . .132164, 133863 . .134018 . .135022 . .135075 . .135890 . .135980, 137445 . .137599 . .138436 . .138610 . .139077 . .>139255.) |
| gene | /product="lactoferrin" /note="confirmed by similarity to lactoferrin protein" /codon_start=1 /evidence="not_experimental" /product="lactoferrin" /protein_id="AAAB57795.1" /db_xref="GT:2104522" /translation="DJSDEAERDEYEELCLCPDNTRPKVDFKDCHLARVSHAVARS NGKEDAIWNRLRQAEKEGDKSPSFGDKSPFOLGKSPSFGDKSPFOLGKSPFOLG LGCGSYFTATONLKRSEETAAARAVWCGAVLGEQELKRCWCGEGSUSQVSSA TECDTALVIGEADMSLDGYYVTTAGKCGLWVLAENYTSQSSQDDEPNCYDVRPE YLAVALVRRDSTSLTWSVYGGKKSCHTAVTAVTGNMIPMGLNFNGSCDEYESES CAPGSDPNSNLCALCIGDEGENKCPVNPNSNERYVGTAFRCLAEAGDVAEKFDTV LQNTDGNNNDAWDLKLADFLALCLDQKRPVTEARSCHLQVYVAVFVMDKYER LKVYLHQQOKFGRGSDCDKFLQFQSETKNLFLNDNTTECLARLHGKTT*EKYLGPQ |
| BASE COUNT | 41194 a 30122 c 32403 g 39349 t |
| ORIGIN | Query Match 56 .0%; Score 1250 .8; DB 9; Length 143068; Best Local Similarity 99 .8%; Pred. No. 0; Matches 1252; Conserved 0; Mismatches 2; Indels 0; Gaps 0; |
| QY | 979 AGCTCTTTACATAGCTTCTGGCTGTAGATTGCGCCACTCCAAAACCAAGTGTCTGGAA 1038 |
| Db | 48253 AGCTCTTTACATAGCTTCTGGCTGTAGATTGCGCCACTCCAAAACCAAGTGTCTGGAA 48312 |
| QY | 1039 GTCTCAGGAGTGGACAGGAAGAAATCTGTAAGTGTACTACACAGACTCTCGATGGT 1098 |
| Db | 48313 GTCTCAGGAGTGGACAGGAAGAAATCTGTAAGTGTACTACACAGACTCTCGATGGT 48372 |
| QY | 1099 CTGGAAAGGAAGTCAATTGGAGAGGCCCTGAAGCAAGTCTTCAGGACAAAGAGGA 1158 |
| Db | 48373 CTGGAAAGGAAGTCAATTGGAGAGGCCCTGAAGCAAGTCTTCAGGACAAAGAGGA 48432 |
| QY | 1159 GCCTAGAGACAGAAATGAGCAATCTGCTTGTGAAATCACAGCTGGCTCACAGATG 1218 |
| Db | 48433 GCCTAGAGACAGAAATGAGCAACTCTGCTTGTGAAATCACAGCTGGCTCACAGATG 48492 |

| | | | |
|-----|--------|--|--------|
| QY | 1219 | TGTGATTCACAGTGTGAATCTGGTCTAGGTACAGCAGGAGGTGAGGAGAG | 1278 |
| Ddb | 4 8493 | TGTGATTCACAGTGTGAATCTGGTCTAGGTACAGCAGGAGGTGAGGAGAG | 4 8552 |
| QY | 1279 | AGACTTCAGCTGGTGGAAAACACTATTTCACAACTACTCTCCAGTTCATTGTTG | 1338 |
| Ddb | 4 8553 | AGACTTCAGCTGGTGGAAAACAGATTTCACAACTACTCTCCAGTTCATTGTTG | 4 8612 |
| QY | 1339 | AAATACAGGCAATAGAGTTCAGACTTTTAATAATAGTAAAATAAAATTAAAGCTGAAAC | 1398 |
| Ddb | 4 8613 | AAATACAGGCAATAGAGTTCAGACTTTTAATAATAGTAAAATAAAATTAAAGCTGAAAC | 4 8672 |
| QY | 1399 | TGCAACTTGTAAATGTTGAGTTGAGTTGAGTGTACATGTCAAACGTTGAAAT | 1458 |
| Ddb | 4 8673 | TGCAACTTGTAAATGTTGAGTTGAGTGTACATGTCAAACGTTGAAAT | 4 8732 |
| QY | 1459 | GCNTGATTAGTCACAGAGATAATTCTACGTTGAGCTTAAGAATTGAGAGGTGTTAT | 1518 |
| Ddb | 4 8733 | GCNTGATTAGTCACAGAGATAATTCTACGTTGAGCTTAAGAATTGAGAGGTGTTAT | 4 8792 |
| QY | 1519 | GTTTGGGAGACTGCTGAGTCAACCCAAATAGTTGATTGGCAGGAGTTGGAGTGTGTTG | 1578 |
| Ddb | 4 8793 | GTTTGGGAGACTGCTGAGTCAACCCAAATAGTTGATTGGCAGGAGTTGGAGTGTGTTG | 4 8853 |
| Qy | 1579 | ATCTGTGGCACATTAGCCTATGTCATGCCAGCATCTAAAGTAATGATGTCGTTTGAAATCA | 1638 |
| Ddb | 4 8853 | ATCTGTGGCACATTAGCCTATGTCATGCCAGCATCTAAAGTAATGATGTCGTTTGAAATCA | 4 8911 |
| Qy | 1639 | CAGTATACGTCTCAATGCGTGTCAATTGCTGAGTCTCATCTCAGCTGGATCTCATCTCAGGCTGTCGCCA | 1698 |
| Ddb | 4 8913 | CAGTATACGTCTCAATGCGTGTCAATTGCTGAGTCTCATCTCAGGCTGTCGCCA | 4 8971 |
| Qy | 1699 | AAACGCTTGTGTTTTGTTGTATCATTAGATGATGCTGTTTAATCACATTGGAGT | 1758 |
| Ddb | 4 8973 | AAACGCTTGTGTTTTGTTGTATCATTAGATGATGCTGTTTAATCACATTGGAGT | 4 9033 |
| Qy | 1759 | GTTTCAGTGTGCCAGATGTCCTGATGTCATATTGTCCTCATATTGTCCTGAGTGGAA | 1818 |
| Ddb | 4 9033 | GTTTCAGTGTGCCAGATGTCCTGATGTCATATTGTCCTGAGTGGAA | 4 909 |
| Qy | 1819 | CTCCCTAAATCAATTGGCTCTAAATTAAGCTTATGTCCTATTGTAAGAGTGGAG | 1878 |
| Ddb | 4 9093 | CTCCCTAAATCAATTGGCTCTAAATCAAAAGCTTAAACCTTATGGTAAAGAATGGAG | 4 915 |
| Qy | 1879 | GGGGAGAGGCCCCCTGAAAGTAAAGTAAAGCAGACTTCTCTAGTGTGGCCAAAGTTAAAGATG | 1938 |
| Db | 4 9153 | GGGGAGAGGCCCCCTGAAAGTAAAGCAGACTTCTCTAGTGTGGCCAAAGTTAAAGATG | 4 921 |
| Qy | 1939 | TCTCTATGTTGCCAGTGTGTTCTGATGTCAGCAGCAAAACTCTGGCTCTAGA | 1998 |
| Ddb | 4 9213 | TCTCTATGTTGCCAGTGTGTTCTGATGTCAGCAGCAAAACTCTGGCTCTAGA | 4 922 |
| Qy | 1999 | ACCGCCAAACTTGGGAAGTACAGTCTCCAAAGCTGGACTATGGCTTACTTCAGGCCACAT | 2059 |
| Ddb | 4 9273 | ACCGCCAACTTGGGAAGTACAGTCTCCAAAGCTGGACTATGGCTTACTTCAGGCCACAT | 4 933 |
| Qy | 2059 | GGCTAAAGAAGGTTTCAGAAAGAAGTCAATAAGTTAAGTGAATGTAATCTGTT | 2177 |
| Ddb | 4 9333 | GGCTAAAGGTTTCAGAAAGAAGTCAATAAGTTAAGTGAATGTAATCTGTT | 4 944 |
| Qy | 2119 | GTATGATCTTAATGATGTCATAAAATGTTAAGTGAATGTAATCTGTTGATAAAG | 2232 |
| Ddb | 4 9453 | GTATGATCTTAATGATGTCATAAAATGTTAAGTGAATGTAATCTGTTGATAAAG | 4 9506 |

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

| BglII | | EcoRI | | HindIII | | | |
|-----------|-------------|-----------|-------------|-----------|-------------|-------|-------|
| SeqDerMap | FingerPrint | SedDerMap | FingerPrint | SeqDerMap | FingerPrint | | |
| 11786 | 12040 | 8696 | 8837 | 9531 | 9423 | 2546 | 2640 |
| 2067 | 2065 | 6 | <800 | 6382 | 6501 | 6383 | 6450 |
| 5681 | 5720 | 1846 | 1824 | 512 | <800 | 172 | <800 |
| 910 | 897 | 54 | <800 | 10449 | 10229 | 332 | 9107 |
| 3716 | 3953 | 4052 | 3986 | 449 | <800 | 242 | 9107 |
| 875 | 897 | 1159 | 1130 | 6692 | 6501 | <800 | <800 |
| 2215 | 2215 | 560 | <800 | 953 | 1025 | 15571 | 15803 |
| 1705 | 1653 | 2287 | 2267 | 3124 | 3176 | 3564 | 3573 |
| 5763 | 5720 | 4905 | 4891 | 1054 | 1025 | 1157 | 1161 |
| 5844 | 5720 | 3049 | 3078 | 3985 | 3998 | 453 | 453 |
| 5061 | 5001 | 1377 | 1394 | 1100 | 1025 | 3953 | 3953 |
| 2625 | 2640 | 9903 | 9772 | 124 | <800 | 1429 | 1394 |
| 725 | <800 | 1022 | 1021 | 2671 | 2693 | 4478 | 4478 |
| 1173 | 1161 | 12606 | 12503 | 1908 | 1968 | 1369 | 1334 |
| 5747 | 5720 | 866 | 868 | 83 | <800 | 752 | 752 |
| 9995 | 9684 | 9817 | 9772 | 7455 | 7474 | 7881 | 7987 |
| 999 | 999 | 3598 | 3601 | 1305 | 1267 | 1565 | 1565 |
| 4541 | 4503 | 452 | <800 | 1047 | 1025 | 7533 | 7635 |
| 2950 | 2981 | 7549 | 7635 | 3299 | 3301 | 1624 | 1653 |
| 406 | <800 | 2063 | 2075 | 5279 | 5237 | 1653 | 1653 |
| 3375 | 3602 | 5837 | 5858 | 6815 | 6926 | 16442 | 16442 |
| 13024 | 13045 | 13685 | 13328 | 435 | <800 | 16192 | 16192 |
| 416 | <800 | 4104 | 3986 | 2509 | 2576 | 11020 | 10820 |
| 10298 | 10140 | 1943 | 1928 | 2218 | 2172 | 13328 | 13328 |
| 1478 | 1452 | 3964 | 3986 | 3797 | 3802 | 13328 | 13328 |
| 287 | <800 | 2758 | 2771 | 7758 | 7830 | 13306 | 13328 |
| 205 | <800 | 167 | <800 | 16192 | 16442 | 2450 | 8741 |
| 9428 | 9684 | 1307 | 1304 | 11020 | 10820 | 8681 | 8681 |
| 3809 | 3953 | 13306 | 13328 | 1978 | 1968 | 2243 | 2243 |
| 1275 | 1234 | 2423 | 2450 | 8741 | 8681 | 2267 | 2267 |
| 3351 | 3381 | 2243 | 2267 | 4795 | 4815 | 4795 | 4815 |

| | | | | | | |
|------------|--|--|-------|---|--|------------|
| QY | 1219 | TGTGATTACAGTGTGAATCTTGGTGTACGTACCGGAGGGTGGAGGAGG | 1278 | ACCESSION VERSION | G07239 | GI: 860484 |
| Db | 16444 | TGTGATTCAAGTGTGAATCTTGGTGTACGTACCGGAGGGTGGAGGAGG | 16503 | KEYWORDS SOURCE | STS; STS sequence; primer; sequence tagged site. Homo sapiens STSs derived from sequences in dbEST and the Unigene Collection. | |
| QY | 1279 | AGACTCCAGCTGGGGTGGAAAACAGTATTTCAGAACACTTCCAGTCTCAATTGT | 1338 | ORGANISM | Homo sapiens | |
| Db | 16504 | AGACTCCAGCTGGGGTGGAAAACAGTATTTCAGAACACTTCCAGTCTCAATTGT | 16563 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| QY | 1339 | ATAACAGGCAATAGGTCAAGTCTAGCTTTAAATAAAATAAAAGCTGAAAC | 1398 | REFERENCE AUTHORS | 1 (bases 1 to 1068) | |
| Db | 16564 | ATAACAGGCAATAGGTCAAGTCTAGCTTTAAATAAAATAAAAGCTGAAAC | 16623 | TITLE | Whitehead Institute/MIT Center for Genome Research; Physically Mapped ESTs | |
| QY | 1399 | TGCAACTGTAAATGTTGAAAGTTGAGTTGAGTTGCTATCATGCAACCTGAAAT | 1458 | JOURNAL COMMENT | Unpublished (1995) | |
| Db | 16624 | TGCAACTGTAAATGTTGAAAGTTGAGTTGCTATCATGCAACCTGAAAT | 16683 | CONTACT | Thomas Hudson Whitehead Institute/MIT Center for Genome Research 9 Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900 Fax: 617 252 1902 Email: thudson@geneome.wi.mit.edu | |
| QY | 1459 | GCTGTATTAGTCACAGAGATAATTCTAGCTTGAGTTGAGAATTTGAGCAGGNGTAT | 1518 | Primer A: | GGAAATCACAGGTCTGGCTT | |
| Db | 16684 | GCTGTATTAGTCACAGAGATAATTCTAGCTTGAGTTGAGAATTTGAGCAGGNGTAT | 16743 | Primer B: | ACTGTTTCCACCCAGCTG | |
| QY | 1519 | GTTTGGGAGACTGCTGAGTCACCCCATAGTGTGAGGTTGAGTTGAGTGGTGGT | 1578 | Primer Profile: | STS size: 114 | |
| Db | 16744 | GTTTGGGAGACTGCTGAGTCACCCCATAGTGTGAGGTTGAGTGGTGGT | 16803 | Presoak: | | |
| QY | 1579 | ATCTGTGGCACATTACGCTATGCGCATGCAGCATCTAAGTATGTCGTTGATCA | 1638 | Denaturation: | | |
| Db | 16804 | ATCTGTGGCACATTACGCTATGCGCATGCAGCATCTAAGTATGTCGTTGATCA | 16863 | Annealing: | 56 degrees C | |
| QY | 1639 | CACTATAGGCTCCATCGGTGATCTCGAGCTCCTCAGGGCTTGCTGCCA | 1698 | Polymerization: | | |
| Db | 16864 | CACTATAGGCTCCATCGGTGATCTCGAGCTCCTCAGGGCTTGCTGCCA | 16923 | PCR Cycles: | 35 | |
| QY | 1689 | ATCTGTGGCTTCAGATGTCCTGATCTATGTCGCTCATATGTCGTTGCGACT | 1758 | Thermal Cycler: | | |
| Db | 16924 | ATCTGTGGCTTCAGATGTCCTGATCTATGTCGTTGCGTTAACATTCGGAT | 16983 | Protocol: | | |
| QY | 1759 | GTTTCAGAGCTTCAGATGTCCTGATCTATGTCGCTCATATGTCGTTGCGAA | 1818 | Template: | 10 ng | |
| Db | 16984 | GTTTCAGAGCTTCAGATGTCCTGATCTATGTCGTTGCGTTAACATTCGGAT | 17043 | Primer: | each 5 pm | |
| QY | 1819 | CTCCCTAAATCAAATTGGCTCTTAACTCAAGCTTTAACCTTATGTTGGAG | 1878 | dNTPs: | each 4 nM | |
| Db | 17044 | CTCCCTAAATCAAATTGGCTCTTAACTCAAGCTTTAACCTTATGTTGGAG | 17103 | Tag Polymerase: | 0.025 units/ul | |
| QY | 1879 | GTCGAGAACTCCCTGAAGTAAAGCTTCTCTAGTCGAGCCAAAGTAAAGATG | 1938 | Total Vol: | 20 ul | |
| Db | 17104 | GTCGAGAACTCCCTGAAGTAAAGCTTCTCTAGTCGAGCCAAAGTAAAGATG | 17163 | Buffer: | | |
| QY | 1939 | TTCCTATGTTGCCAGTGTCTGATCTGATCTGATCAAGAAAGAACACMGGGCTTCCTAGA | 1998 | MgCl2: | 1.5 mM | |
| Db | 17164 | TTCCTATGTTGCCAGTGTCTGATCTGATCTGATCAAGAAAGAACACMGGGCTTCCTAGA | 17223 | KCl: | 50 mM | |
| QY | 1999 | ACCAGGCAACUTGGGAACTAGACTCCAACTGGGACTATGGCTCTACTTCAGGCCACAT | 2058 | Tris-HCl: | 10 mM | |
| Db | 17224 | ACCAGGCAACUTGGGAACTAGACTCCAACTGGGACTATGGCTCTACTTCAGGCCACAT | 17283 | pH: | 9.3 | |
| QY | 2059 | GGCTAAAGAAGGTTCAGAAAGAAGTGGGACAGACGAAACTTCACCTTCATATA | 2118 | FEATURES | Prepared with primer pairs derived from U03982 -- Unigene. | |
| Db | 17284 | GGCTAAAGAAGTGGGAAACAGTATTTCAGAAGAAGTGGGACAGACGAAACTTCACCTTCATATA | 17343 | source | Location/Qualifiers | |
| QY | 2119 | GTTATGTCCTTAATGTAATGCTATAAAATGTTAAAGTTGAGGTGATGAAATGTAATAGTGT | 2178 | 1: 1.068 | | |
| Db | 17344 | GTTATGTCCTTAATGTAATGCTATAAAATGTTAAAGTTGAGGTGATGAAATGTAATAGTGT | 17403 | /db_xref="taxon:9606" | | |
| QY | 2179 | TPTAACACTATGTTGGAAATAATACTCAATGCTATAACTATGTTGGGATGAAATGTTGG | 2232 | /map="730_D_5"; 913_C_5; 941_A_7; 743_H_10; 781_B_10; | | |
| Db | 17404 | TPTAACACTATGTTGGAAATAATACTCAATGCTATAACTATGTTGGGATGAAATGTTGG | 17457 | STS | | |
| QY | 2235 | CACCTGGTTGGGGTGGGGAAACAGTATTTCCTAACACTCCCTTCAGTTCAGTTCAGT | 1344 | primer_bind | | |
| Db | 121 | CACCTGGTTGGGGAAACAGTATTTCCTAACACTCCCTTCAGTTCAGTTCAGTTCAGT | 120 | primer_bind | | |
| RESULT | 8 | | | complement(121..140) | | |
| G07239 | G07239 | | | 329 t | | |
| LOCUS | human STS WI-9314 | 1068 bp | DNA | 328 g | | |
| DEFINITION | human STS WI-9314, sequence tagged site. | | | 329 t | | |

| AUTHORS | Charo, I. F. and Coughlin, S. R. |
|---|--|
| TITLE | Recombinant mammalian monocyte chemotactic protein-1 (MCP-1) |
| JOURNAL | Receptors (MCP-1R, CCR-2) |
| FEATURES | Patent: US 6132987 A 3 17-OCT-2000; |
| source | Location/Qualifiers 1. .1979 /organism="unknown" |
| BASE COUNT | 530 a 451 c 563 t |
| ORIGIN | |
| Query Match | 43.9%; Score 980; DB 6; Length 1979; |
| Best Local Similarity | 100.0%; Pred. No. 7.9e-250; |
| Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0 | |
| Py | 1 GGATTCACAGGAGCAATTCCAGTACATCCACACATGCTGCCACATCGTTC 60 |
| Db | 2 GGATTCACAGGAGCAATTCCAGTACATCCACACATGCTGCCACATCGTTC 101 |
| Py | 61 CGGTTATCGAAATACCAAGAGGGTGAAGAGTCACCCACCTTTGATTATGAT 120 |
| Db | 102 CGGTTATCGAAATACCAAGAGGGTGAAGAGTCACCCACCTTTGATTATGAT 161 |
| Py | 121 TACGGTGTCTCCCTGTCAAAATTGACGTCGAAGCAAAATTGGGCCAAC 180 |
| Db | 162 TACGGTGTCTCCCTGTCAAAATTGACGTCGAAGCAAAATTGGGCCAAC 221 |
| Y | 181 CTCTACTCGCTGGTGTTCATCTTGGTGTCAATTGACGTCGAAGCAAAATTGGGCCAAC 240 |
| Y | 222 CTCTACTCGCTGGTGTTCATCTTGGTGTCAATTGACGTCGAAGCAAAATTGGGCCAAC 281 |
| Y | 241 ATAAACTGCAAAAGCTGAACTTGTACTGACATTACCTGTCACACTGGCCATCT 300 |
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| Y | 301 GATCAGCTTTCCTTCTTAACTCTCCATTGTTGGCTCATCTGCAAAATTGAGGGTC 360 |
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| b | 402 TTGGGAATGGAAATGGCAAAATTGACAGGGCTGTATCACATCGGTATTGTCGGGA 461 |
| Y | 421 ATCTCTTCATCATCTCCCTCAAACTGATAGACCTTGGCTATTGTCCTGGCTT 480 |
| o | 462 ATCTCTTCATCATCTCCCTCAAACTGATAGACCTTGGCTATTGTCCTGGCTT 521 |
| Y | 481 GCTTTAAAGCCAGACGGTACCTTGGGTTGGTACAAAGTGTACCTGGTTGGT 540 |
| o | 522 GCTTTAAAGCCAGACGGTACCTTGGGTTGGTACAAAGTGTACCTGGTTGGT 581 |
| Y | 541 GCTGTGTTGCTCTGTCTGCCAGGAATCATCTTAACTTAATGGCAAGAAGATTCGT 600 |
| o | 582 GCTGTGTTGCTCTGTCTGCCAGGAATCATCTTAACTTAATGGCAAGAAGATTCGT 641 |
| Y | 601 TATGTCGTCGCCCCATTGTTCCAGGAGTGGAAATTCCACACAAATGGGAC 660 |
| o | 642 TATGTCGTCGCCCCATTGTTCCAGGAGTGGAAATTCCACACAAATGGGAC 701 |
| Y | 661 ATTTGGGGCTGGCTGCTGCCCTGCTGCTCATCTGGTCACTCGCTACTCGGAAATCCTGAAA 720 |
| o | 702 ATTTGGGGCTGGCTGCTGCCCTGCTGCTCATCTGGTCACTCGCTACTCGGAAATCCTGAAA 761 |
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| o | 762 ACCCTGCTGGGCTGACTTCTGGACTCCCTCATCTGGTCACTCGCTACTCGGAAATCCTGAAA 881 |
| Y | 781 ATCATGATGGTGTACTTCTGACTTCTGGACTCCCTCATCTGGTCACTCGCTACTCGGAAATCCTGAAA 900 |
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| BASE COUNT ORIGIN | 530 a | 435 c | 451 g | 563 t |
|-----------------------|--------|--|---------------|-----------|
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| Db | 42 | GGATGAAAGGAGCCATTCCCCAGTACATCCACACATGGTGTCCACATCGTGTCT | 101 | |
| Qy | 61 | CGGTTATCAGAAATACCAGAGACCGTGAAGAACTCACCCTTTTGTATTGAT | 120 | |
| Db | 102 | CGGTTATCAGAAATACCAGAGACCGTGAAGAACTCACCCTTTTGTATTGAT | 161 | |
| Qy | 121 | TACGGTGTCTCTGTCATAAATTGACGTGAAGCAAATTGGGGCCAAACTCCCGCCCTCG | 180 | |
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| Qy | 181 | CTCTACTCCCTGGGTGTCTACTTGGGTGTGGCAACATGCTGGTCCTCATCTTA | 240 | |
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| Qy | 241 | ATAACTGCAAAGCTGAAGTGTGTCATGACATTACCTGCTAACCTGCCATCTCT | 300 | |
| Db | 282 | ATAACTGCAAAGCTGAAGTGTGTCATGACATTACCTGCTAACCTGCCATCTCT | 341 | |
| Qy | 301 | GATCTGCTTTCTTATRACTCTCCATGTTGGGTGTCATGTGCTCAACCTGGCT | 360 | |
| Db | 342 | GATCTGCTTTCTTATRACTCTCCATGTTGGGTGTCATGTGCTCAACCTGGCT | 401 | |
| Qy | 361 | TTGGGAATGCAATGTAATTACAGGGCTGATACATGGTTATTTGGGGAA | 420 | |
| Db | 402 | TTGGGAATGCAATGTTGACTGACATTACAGGGCTGATACATGGTTATTTGGGGAA | 461 | |
| Qy | 421 | ATCTCTCATGATCCCTCTGACATGATGACATCTGGCTACTGGTGTGTT | 480 | |
| Db | 462 | ATCTCTCATGATCCCTCTGACATGATGACATCTGGCTACTGGTGTGTT | 521 | |
| Qy | 481 | GCTTTAAAGCCAGGAGGTCACTTGGGTGGTACAGTGATCACCTGGTGTG | 540 | |
| Db | 522 | GCTTTAAAGCCAGGAGGTCACTTGGGTGGTACAGTGATCACCTGGTGTG | 581 | |
| Qy | 541 | GCTGCTGTTGCTCTGCCCCATGAAATCATCTACTAAATGCCAGAAAGGATCTGTT | 600 | |
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| Qy | 601 | TATGCTGCTGCCCCATGAAATCATCTACTAAATGCCAGAAACATAATGAGGAAC | 660 | |
| Db | 642 | TATGCTGCTGCCCCATGAAATCATCTACTAAATGCCAGAAACATAATGAGGAAC | 701 | |
| Qy | 661 | ATTTGGGCTGTCCTGCTGCTCATGGTCACTCGGGAAATCTGCAA | 720 | |
| Db | 702 | ATTTGGGCTGTCCTGCTGCTCATGGTCACTCGGGAAATCTGCAA | 761 | |
| Qy | 721 | ACCCGCTGCTGCTGAAAGCAGAGAAAGGGCATAGGGCAACTGGACAAAGCCACG | 780 | |
| Db | 762 | ACCCGCTGCTGCTGAAAGCAGAGAAAGGGCATAGGGCAACTGGACAAAGCCACG | 821 | |
| Qy | 781 | ATCATGATGTTTACTTCTGACTCCCTATAACATGTCATCTCTGAAACACC | 840 | |
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| QY | 901 | CAGGTGACAGAGACTCTGGGTAGACCTCACTGCTGACATCACATCTATGCCCTC | 960 |
| Db | 942 | CAGGTGACAGAGACTCTGGGTAGACCTCACTGCTGACATCACATCTATGCCCTC | 1001 |
| QY | 961 | GTTGGGGAGAAGTTCAGAG | 980 |
| Db | 1002 | GTTGGGGAGAAGTTCAGAG | 1021 |

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| AUTHORS | Yamagami, S. | Db | 481 | AGTGTGATCACCTGGCATCTGGTGGCTTGGCTCTGCCCCAGGAATCATCTTACTAA | 540 |
| TITLE | Submitted (22-Apr-1994) Shinsuke Yamagami, TRUJIN LIMITED, | Qy | 580 | TGCAGAAAGAGATCTGTTATTCGCCCCATTATTCACAGGATGGAATA | 639 |
| JOURNAL | Institute for Bio-Medical Research; 4-3-2, Asahigaoka, Hino, Tokyo | Db | 541 | TGCCAGAAAGATCTGTTATTCGCCCCATTATTCACAGGATGGAATA | 600 |
| COMMENT | 191, Japan (Tel:0425-86-8282) | Qy | 640 | TTCACACACATAATGAGGAACATTTGGGGTGTCTGGCGTGTCTCATGGTCAT | 699 |
| | Submitted (22-Apr-1994) to DDBJ by: | Db | 601 | TCCACACATAATGAGGAACATTTGGGGTGTCTGGCGTGTCTCATGGTCAT | 660 |
| | Shinsuke Yamagami | Qy | 700 | TGCTACTCGGGAACTCTGAAACCTGCTGGTGTGAAACGAGAGAAAGGCCATGG | 759 |
| | TruJin Limited | Db | 661 | TGCTACTCGGGAACTCTGAAACCTGCTGGTGTGAAACGAGAGAAAGGCCATGG | 720 |
| | Institute for Bio-Medical Research | Qy | 760 | GCATGAGAGTCATCCTACATTGATGTTACTTTCTCTGGACTCCATAAC | 819 |
| | 4-3-2 Asahigaoka | Db | 721 | GCATGAGAGTCATCCTACATTGATGTTACTTTCTCTGGACTCCATAAC | 780 |
| | Hino, Tokyo 191 | Qy | 820 | ATTTGTCATTCCTCCGAAACACTTCAGGATTCCTGGCCCTGAACTGAAAGCACC | 879 |
| FEATURES | Phone: 0425-86-8282 | Db | 781 | ATTTGTCATTCCTCCGAAACACTTCAGGATTCCTGGCCCTGAACTGAAAGCACC | 840 |
| Source | Fax: 0425-87-512. | Qy | 880 | AGTAACTGACCCAGCCACGCAAGTGACAGAGACTCTGGGATGACTACTGTCAT | 939 |
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| | FYRETVDVTSNTSPQEVSAGL" | REFERENCE | | | |
| BASE COUNT | 255 a 259 c 247 g 322 t | AUTHORS | | | |
| ORIGIN | | AUTHORS | | | |
| | | Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L. | | | |
| Query Match | 42.1% | TITLE | | | |
| Best Local Similarity | 99.9% | NON-ENDEOGENOUS, constitutively activated known g protein-coupled | | | |
| Matches | 940; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | RECEPTORS | | | |
| Db | 1 ATGCTGTCACATCTCGTTCTCGGTTATCAGAAATAACANAGAGCGTGANAGTC | JOURNAL | | | |
| Qy | 40 ACCACCTTTTGTGATTATGATTACGCGTCTCCCTGTATAATTGAGGTGAAATA | FEATURES | | | |
| Db | 1 ATGCTGTCACATCTCGTTCTCGGTTATCAGAAATAACAAACGAGCGTGANAGTC | source | | | |
| Qy | 100 ACCACCTTTTGTGATTATGATTACGCGTCTCCCTGTATAATTGAGGTGAAATA | ORIGIN | | | |
| Db | 61 ACCACCTTTTGTGATTATGATTACGCGTCTCCCTGTATAATTGAGGTGAAATA | Query Match | | | |
| Qy | 160 GGGCCCACACTCTGGCTCGCTACTCGCGTCTACTCTGGCTCTACTCTGGCT | Best Local Similarity | | | |
| Db | 121 GGGCCCACACTCTGGCTCTACTCTGGCTCTACTCTGGCTCTACTCTGGCT | Matches | 939; conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
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| Qy | 340 TCTGCTGCAAATGAGTGGCTTCTGGAAATGCAATTTCTCATCTGGCTCA | Qy | 40 ATGCTGTCACATCTCGCTCTCGCTTCTGCTTCTGCTTCTGCTTCTGCT | | |
| Db | 301 TCTGCTGCAAATGAGTGGCTTCTGGAAATGCAATTTCTCATCTGGCTCA | Db | 1 ATGCTGTCACATCTCGCTCTCGCTTCTGCTTCTGCTTCTGCTTCTGCT | | |
| Qy | 400 CACATCGTTATTTCGGAAATCTCATCTGGCTCA | Qy | 100 ACCACCTTTGTGATGATGTTGCTTCTCATCTGGCTCA | | |
| Db | 361 CACATCGTTATTTCGGAAATCTCATCTGGCTCA | Db | 61 ACCACCTTTGTGATGATGTTGCTTCTCATCTGGCTCA | | |
| Qy | 460 GCTATTGTCATGCTGTTGCTTAAAGCCAGGACGCTCACCTTGGGTGGTGA | Qy | 160 GGCCCAACTCTGGCTCTACTCGCTGCTGTTCTCATCTGGCTCA | | |
| Db | 421 GCTATTGTCATGCTGTTGCTTAAAGCCAGGACGCTCACCTTGGGTGGTGA | Db | 121 GGCCCAACTCTGGCTCTACTCGCTGCTGTTCTCATCTGGCTCA | | |
| Qy | 520 AGTGTGATCACCCGTTGGCTGTTGCTTCTGTCAGGAAATCATCTTACTAA | Qy | 220 ATGCTGTCGTCATCTTAAACTGCAAAAGCTGAATGTTGACTGACATTAC | | |

| | | | | |
|----|-----|---|----------------------|-----|
| Db | 181 | ATGCTGGTCCATCTTAATAAACTGCAAAAGCTGAACTGCTTGA | ACTGACATTAC | 240 |
| Qy | 280 | CTGCTAACCTGGCCATCTGATCTGCTTCTCTATCTCCATCTG | GGCTCAC | 339 |
| Db | 241 | CTGCTAACCTGGCCATCTGCTTCTCTATCTCCATCTGGCTCAC | | 300 |
| Qy | 340 | TCTGCTGAAATGAGGGCTTGGAAATGCAATGCA | AAATTATCAGGGCTGAT | 399 |
| Db | 301 | TCTGCTGAAATGAGGGCTTGGAAATGCAATGCA | AAATTATCAGGGCTGAT | 360 |
| Qy | 400 | CACATCGGTTATTGGCGGAATCTCTCATCCTCTGACAACTG | ATGATACCTG | 459 |
| Db | 361 | CACATCGGTTATTGGCGGAATCTCTCATCCTCTGACAACTGAT | ACATCCCTG | 420 |
| Qy | 460 | GCTATGTCCTCCTGCTGTTGCTTAAAGCAGGACGGTAC | CCCTTGCTGACA | 519 |
| Db | 421 | GCTATGTCCTCCTGCTTAAAGCAGGACGGTAC | CCCTTGCTGACA | 480 |
| Qy | 520 | AGTGTGATCACCTGGTGTGCTTCTCTCCAGGAATCATCTT | TACTAA | 579 |
| Db | 481 | AGTGTGATCACCTGGTGTGCTTCTCTCCAGGAATCATCTT | TACTAA | 540 |
| Qy | 580 | TGCCAGAAGAAAGATCTGTTATGCTGTCGCCCTATTTTC | CACAGGATGGAATAAT | 639 |
| Db | 541 | TGCCAGAAGAAAGATCTGTTATGCTGTCGCCCTATTTTC | CACAGGATGGAATAAT | 600 |
| Qy | 640 | TTGCCACACATAATGAGAACATTGGGGTGCCTCATGGT | TCATGGTAC | 699 |
| Db | 601 | TTGCCACACATAATGAGAACATTGGGGTGCCTCATGGT | TCATGGTAC | 660 |
| Qy | 700 | TGCTACTGGAAATCCTGAAACCCCTGGTCTGGT | CGCTCTGCTGTCATCGTCAT | 759 |
| Db | 661 | TGCTACTGGAAATCCTGAAACCCCTGGTCTGGT | CGCTCTGCTGTCATCGTCAT | 720 |
| Qy | 760 | GCACTGAGACTCATCTTACCATCATGATTTGTTACTT | CTCTGGA | 819 |
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| Qy | 820 | AGTCAACTGGACCAAGCACCGAGCTGAGAGACTCTGG | ATGACTGTCATGTC | 939 |
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| Qy | 940 | AATCCCATCATCTATGCTCTGTTGGGAGGTCAGAG | 950 | |
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 Job time : 5958.75 secs

